



# SEQUENCE LISTING

<110> Goodman, Corey S.  
Kidd, Thomas  
Mitchell, Kevin J.  
Tear, Guy  
The Regents of the University of California

<120> ROBO: A Novel Family of Polypeptides and Nucleic Acids

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<141> 2004-04-16

<150> US 60/062,921  
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<220>
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Pro Thr Ile Gln Trp Phe Lys Asp Gly Arg Glu Leu Lys Thr Asp Thr
 35                      40                      45

Gly Ser His Arg Ile Met Leu Pro Ala Gly Gly Leu Phe Phe Leu Lys
 50                      55                      60

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Val	Ile	His	Ser	Arg	Arg	Glu	Ser	Asp	Ala	Gly	Thr	Tyr	Trp	Cys	Glu	65	70	75	80
Ala	Lys	Asn	Glu	Phe	Gly	Val	Ala	Arg	Ser	Arg	Asn	Ala	Thr	Leu	Gln	85	90	95	
Val	Ala	Val	Leu	Arg	Asp	Glu	Phe	Arg	Leu	Glu	Pro	Ala	Asn	Thr	Arg	100	105	110	
Val	Ala	Gln	Gly	Glu	Val	Ala	Leu	Met	Glu	Cys	Gly	Ala	Pro	Arg	Gly	115	120	125	
Ser	Pro	Glu	Pro	Gln	Ile	Ser	Trp	Arg	Lys	Asn	Gly	Gln	Thr	Leu	Asn	130	135	140	
Leu	Val	Gly	Asn	Lys	Arg	Ile	Arg	Ile	Val	Asp	Gly	Gly	Asn	Leu	Ala	145	150	155	160
Ile	Gln	Glu	Ala	Arg	Gln	Ser	Asp	Asp	Gly	Arg	Tyr	Gln	Cys	Val	Val	165	170	175	
Lys	Asn	Val	Val	Gly	Thr	Arg	Glu	Ser	Ala	Thr	Ala	Phe	Leu	Lys	Val	180	185	190	
His	Val	Arg	Pro	Phe	Leu	Ile	Arg	Gly	Pro	Gln	Asn	Gln	Thr	Ala	Val	195	200	205	
Val	Gly	Ser	Ser	Val	Val	Phe	Gln	Cys	Arg	Ile	Gly	Gly	Asp	Pro	Leu	210	215	220	
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Arg	Lys	Phe	Ser	Trp	Leu	His	Ser	Ala	Ser	Gly	Arg	Val	His	Val	Leu	245	250	255	
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Glu	Tyr	Thr	Cys	Glu	Ala	Asp	Asn	Ala	Val	Gly	Gly	Ile	Thr	Ala	Thr	275	280	285	
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Thr	Pro	Glu	Gly	Arg	Ser	Val	Leu	Ser	Ile	Ala	Arg	Phe	Ala	Arg	Glu	355	360	365	
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Tyr	Val	Ile	Glu	Met	Phe	Gly	Lys	Asn	Glu	Thr	Asp	Gly	Trp	Val	Ala		545	550	555
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Leu	Ser	Leu	Pro	Ser	Pro	Met	Ser	Glu	Pro	Ile	Thr	Val	Gly	Thr	Arg		595	600	605
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Ser	Gly	Asp	Val	Val	Glu	Leu	Ser	Asn	Ala	Ser	Val	Val	Asp	Ser	Thr		625	630	635
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Phe	Tyr	Val	Tyr	Ala	Arg	Gln	Leu	Pro	Asn	Pro	Ile	Val	Asn	Asn	Pro		660	665	670
Ala	Pro	Val	Thr	Ser	Asn	Thr	Asn	Pro	Leu	Leu	Gly	Ser	Thr	Ser	Thr		675	680	685
Ser	Ala	Ser	Ala	Ser	Ala	Ser	Ala	Ser	Ala	Leu	Ile	Ser	Thr	Lys	Pro		690	695	700

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<213> *Caenorhabditis elegans*

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<223> *C. elegans* roundabout (robo) cDNA

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Ile Glu His Pro Ile Asp Val Val Val Ser Arg Gly Ser Pro Ala Thr
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Leu Asn Cys Gly Ala Lys Pro Ser Thr Ala Lys Ile Thr Trp Tyr Lys
      50              55              60

Asp Gly Gln Pro Val Ile Thr Asn Lys Glu Gln Val Asn Ser His Arg
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Ile Val Leu Asp Thr Gly Ser Leu Phe Leu Leu Lys Val Asn Ser Gly
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Lys Asn Gly Lys Asp Ser Asp Ala Gly Ala Tyr Tyr Cys Val Ala Ser
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Asn Glu His Gly Glu Val Lys Ser Asn Glu Gly Ser Leu Lys Leu Ala
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Met Leu Arg Glu Asp Phe Arg Val Arg Pro Arg Thr Val Gln Ala Leu
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Pro	Val	Asp	Arg	Ser	Asp	Ser	Gly	Thr	Tyr	Gln	Cys	Val	Ala	Asn	Asn	195	200	205	
Met	Val	Gly	Glu	Arg	Val	Ser	Asn	Pro	Ala	Arg	Leu	Ser	Val	Phe	Glu	210	215	220	
Lys	Pro	Lys	Phe	Glu	Gln	Glu	Pro	Lys	Asp	Met	Thr	Val	Asp	Val	Gly	225	230	235	240
Ala	Ala	Val	Leu	Phe	Asp	Cys	Arg	Val	Thr	Gly	Asp	Pro	Gln	Pro	Gln	245	250	255	
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Cys	Thr	Leu	Val	Gly	Gln	Pro	Ser	Pro	Ala	Tyr	Phe	Trp	Ser	Lys	Glu	340	345	350	
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Val	Asp	Glu	Gly	Ala	Tyr	Val	Cys	Ala	Gly	Met	Asn	Ser	Ala	Gly	Ser	385	390	395	400
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Val	Gln	Lys	Lys	Lys	Ser	Lys	Met	Gly	Lys	Gln	Lys	Gln	Lys	Asn	Val	420	425	430	
Gln	Ser	Ile	Ile	Lys	Tyr	Leu	Ile	Ser	Ala	Val	Thr	Gly	Asn	Thr	Pro	435	440	445	
Ala	Lys	Pro	Pro	Pro	Thr	Ile	Glu	His	Gly	His	Gln	Asn	Gln	Thr	Leu	450	455	460	

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 Asn Ser Met Asp Val Leu Thr Ala Glu Ala Pro Pro Ser Leu Pro Pro  
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Glu	Asp	Val	Arg	Ile	Arg	Met	Leu	Asn	Leu	Thr	Thr	Leu	Arg	Ile	Ser	785	790	795	800
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Gln	Ile	Val	Ile	Val	Gly	Gln	Ala	Pro	Asn	Asn	Asn	Arg	Asn	Ile	Thr	820	825		830
Thr	Asn	Glu	Arg	Ala	Ala	Ser	Val	Thr	Leu	Phe	His	Leu	Val	Thr	Gly	835	840		845
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Lys	His	Leu	Ala	Ala	Gln	Gln	Glu	Asn	Glu	Ser	Phe	Leu	Tyr	Gly	Leu	885	890		895
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Lys	Met	Leu	Arg	Ala	Pro	Ala	Met	Pro	Thr	Asn	Pro	Val	Pro	Pro	Glu	1060	1065		1070
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Asp Val Glu Arg Gly Asn Asp His Gly Thr Pro Ile Pro Thr Ser Asp
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Asn Asp Asp Asn Ser Leu Gly Tyr Thr Gly Ser Arg Leu Arg Gln Glu
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Asp Phe Pro Pro Arg Ile Val Glu His Pro Ser Asp Leu Ile Val Ser
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Lys Gly Glu Pro Ala Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr
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Pro Thr Ile Glu Trp Tyr Lys Gly Gly Glu Arg Val Glu Thr Asp Lys
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Asp Asp Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe
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Phe Leu Arg Ile Val His Gly Arg Lys Ser Arg Pro Asp Glu Gly Val
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Tyr Val Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser His Asn
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Ala Ser Leu Glu Val Ala Ile Leu Arg Asp Asp Phe Arg Gln Asn Pro
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Ser Asp Val Met Val Ala Val Gly Glu Pro Ala Val Met Glu Cys Gln
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Pro Pro Arg Gly His Pro Glu Pro Thr Ile Ser Trp Lys Lys Asp Gly
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Ser Pro Leu Asp Asp Lys Asp Glu Arg Ile Thr Ile Arg Gly Gly Lys
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Pro Val Val Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr Asp Arg  
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 Ser Ser Asp Arg Lys Gly Ser Ser Tyr Lys Gly Arg Glu Val Leu Asp  
 1525 1530 1535  
 Gly Arg Gln Val Val Asp Met Arg Thr Asn Pro Gly Asp Pro Arg Glu  
 1540 1545 1550  
 Ala Gln Glu Gln Gln Asn Asp Gly Lys Gly Arg Gly Asn Lys Ala Ala  
 1555 1560 1565  
 Lys Arg Asp Leu Pro Pro Ala Lys Thr His Leu Ile Gln Glu Asp Ile  
 1570 1575 1580  
 Leu Pro Tyr Cys Arg Pro Thr Phe Pro Thr Ser Asn Asn Pro Arg Asp  
 1585 1590 1595 1600  
 Pro Ser Ser Ser Ser Ser Met Ser Ser Arg Gly Ser Gly Ser Arg Gln  
 1605 1610 1615  
 Arg Glu Gln Ala Asn Val Gly Arg Arg Asn Ile Ala Glu Met Gln Val  
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 Thr Glu Ser  
 1650

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 <213> Homo sapiens  
  
 <220>  
 <223> human roundabout (robo) 2 partial cDNA

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 cagcccaaca gtagatgtc agtgtcacca actggagacc tcacaatcac caacattcaa 180  
 cgttccgacg cgggttacta catctgccag gctttaaactg tggcaggaag catttttagca 240  
 aaagctcaac tggaggttac tgatgttttg acagatagac ctccacctat aattctacaa 300  
 ggcccagcca accaaacgct ggcagtggat ggtacagcgt tactgaaatg taaagccact 360  
 ggtgatcctc ttctgtaat tagctgggta aaggagggat ttacttttcc gggtagagat 420  
 ccaagagcaa caattcaaga gcaaggcaca ctgcagatta agaatttacg gatttctgat 480  
 actggcactt atacttgtgt ggctacaagt tcaagtggag aggcttcctg gagtgcagtg 540  
 ctggatgtga cagagtctgg agcaacaatc agtaaaaact atgatttaag tgacctgcca 600  
 gggccaccat ccaaaccgca agtcactgat gttactaaga acagtgtcac cttgtcctgg 660  
 cagccaggta cccttgaac ccttcagca agtgcatata tcattgaggc tttcagccaa 720  
 tcagtgagca acagctggca gaccgtggca aaccatgtaa agaccaccct ctatactgta 780  
 agaggactgc ggccaatac aatctactta ttcatgtgtca gagcgatcaa cccaaggtg 840  
 tcagtgaccc aagt 854

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 <212> PRT  
 <213> Homo sapiens

<220>

<223> human roundabout (robo) 2 (H2) protein

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			20					25					30			
Leu	Leu	Phe	Pro	Asn	Gln	Pro	Gln	Gln	Pro	Asn	Ser	Arg	Cys	Ser	Val	
		35					40					45				
Ser	Pro	Thr	Gly	Asp	Leu	Thr	Ile	Thr	Asn	Ile	Gln	Arg	Ser	Asp	Ala	
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Gly	Tyr	Tyr	Ile	Cys	Gln	Ala	Leu	Thr	Val	Ala	Gly	Ser	Ile	Leu	Ala	
65					70					75					80	
Lys	Ala	Gln	Leu	Glu	Val	Thr	Asp	Val	Leu	Thr	Asp	Arg	Pro	Pro	Pro	
				85					90					95		
Ile	Ile	Leu	Gln	Gly	Pro	Ala	Asn	Gln	Thr	Leu	Ala	Val	Asp	Gly	Thr	
			100					105					110			
Ala	Leu	Cys	Lys	Cys	Lys	Ala	Thr	Gly	Asp	Pro	Leu	Pro	Val	Ile	Ser	
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Trp	Leu	Lys	Glu	Gly	Phe	Thr	Phe	Pro	Gly	Arg	Asp	Pro	Arg	Ala	Thr	
	130					135					140					
Ile	Gln	Glu	Gln	Gly	Thr	Leu	Gln	Ile	Lys	Asn	Leu	Arg	Ile	Ser	Asp	
145					150					155					160	
Thr	Gly	Thr	Tyr	Thr	Cys	Val	Ala	Thr	Ser	Ser	Ser	Gly	Glu	Ala	Ser	
				165					170					175		
Trp	Ser	Ala	Val	Leu	Asp	Val	Thr	Glu	Ser	Gly	Ala	Thr	Ile	Ser	Lys	
			180					185					190			
Asn	Tyr	Asp	Leu	Ser	Asp	Leu	Pro	Gly	Pro	Pro	Ser	Lys	Pro	Gln	Val	
		195					200					205				
Thr	Asp	Val	Thr	Lys	Asn	Ser	Val	Thr	Leu	Ser	Trp	Gln	Pro	Gly	Thr	
	210					215					220					
Pro	Gly	Thr	Leu	Pro	Ala	Ser	Ala	Tyr	Ile	Ile	Glu	Ala	Phe	Ser	Gln	
225					230					235					240	
Ser	Val	Ser	Asn	Ser	Trp	Gln	Thr	Val	Ala	Asn	His	Val	Lys	Thr	Thr	
				245					250					255		
Leu	Tyr	Thr	Val	Arg	Gly	Leu	Arg	Pro	Asn	Thr	Ile	Tyr	Leu	Phe	Met	
			260					265					270			
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 gtgtccacag acagcaacat gagtgtgtgt gtgatccaga aagccagacc cgccaagaag 180  
 cagaaacacc agccaggaca tctgcgcagg gaagcctacg cagatgatct tccaccccct 240  
 ccagtgccac cacctgctat aaaatcgccc actgtccagt ccaaggcaca gctggaggta 300  
 cggcctgtca tgggtccaaa actcgcgtct atagaagcaa ggacagatag atcgtcagac 360  
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 cgaacaaatc caagtgaccc caga 444

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<220>  
 <223> mouse roundabout (robo) 1 protein

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           20                  25                  30  
 Gln Cys Pro Arg Pro Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser  
           35                  40                  45  
 Ala Val Val Ile Gln Lys Ala Arg Pro Ala Lys Lys Gln Lys His Gln  
   50                  55                  60  
 Pro Gly His Leu Arg Arg Glu Ala Tyr Ala Asp Asp Leu Pro Pro Pro  
   65                  70                  75                  80  
 Pro Val Pro Pro Pro Ala Ile Lys Ser Pro Thr Val Gln Ser Lys Ala  
           85                  90                  95  
 Gln Leu Glu Val Arg Pro Val Met Val Pro Lys Leu Ala Ser Ile Glu  
          100                 105                 110  
 Ala Arg Thr Asp Arg Ser Ser Asp Arg Lys Gly Gly Ser Tyr Lys Gly  
   115                 120                 125  
 Arg Glu Ala Leu Asp Gly Arg Gln Val Thr Asp Leu Arg Thr Asn Pro  
   130                 135                 140  
 Ser Asp Pro Arg  
 145

<210> 13  
 <211> 909  
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 <213> Caenorhabditis elegans

<220>  
 <223> C. elegans roundabout (robo) (CE) protein

<400> 13

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      20           25           30

Ile Ile Glu His Pro Ile Asp Val Val Val Ser Arg Gly Ser Pro Ala
      35           40           45

Thr Leu Asn Cys Gly Ala Lys Pro Ser Thr Ala Lys Ile Thr Trp Tyr
      50           55           60

Lys Asp Gly Gln Pro Val Ile Thr Asn Lys Glu Gln Val Asn Ser His
      65           70           75           80

Arg Ile Val Leu Asp Thr Gly Ser Leu Phe Leu Leu Lys Val Asn Ser
      85           90           95

Gly Lys Asn Gly Lys Asp Ser Asp Ala Gly Ala Tyr Tyr Cys Val Ala
      100           105           110

Ser Asn Glu His Gly Glu Val Lys Ser Asn Glu Gly Ser Leu Lys Leu
      115           120           125

Ala Met Leu Arg Glu Asp Phe Arg Val Arg Pro Arg Thr Val Gln Ala
      130           135           140

Leu Gly Gly Glu Met Ala Val Leu Glu Cys Ser Pro Pro Arg Gly Phe
      145           150           155           160

Pro Glu Pro Val Val Ser Trp Arg Lys Asp Asp Lys Glu Leu Arg Ile
      165           170           175

Gln Asp Met Pro Arg Tyr Thr Leu His Ser Asp Gly Asn Leu Ile Ile
      180           185           190

Asp Pro Val Asp Arg Ser Asp Ser Gly Thr Tyr Gln Cys Val Ala Asn
      195           200           205

Asn Met Val Gly Glu Arg Val Ser Asn Pro Ala Arg Leu Ser Val Phe
      210           215           220

Glu Lys Pro Lys Phe Glu Gln Glu Pro Lys Asp Met Thr Val Asp Val
      225           230           235           240

Gly Ala Ala Val Leu Phe Asp Cys Arg Val Thr Gly Asp Pro Gln Pro
      245           250           255

Gln Ile Thr Trp Lys Arg Lys Asn Glu Pro Met Pro Val Thr Arg Ala
      260           265           270
  
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Tyr Ile Ala Lys Asp Asn Arg Gly Leu Arg Ile Glu Arg Val Gln Pro  
275 280 285  
Ser Asp Glu Gly Glu Tyr Val Cys Tyr Ala Arg Asn Pro Ala Gly Thr  
290 295 300  
Leu Glu Ala Ser Ala His Leu Arg Val Gln Ala Pro Pro Ser Phe Gln  
305 310 315 320  
Thr Lys Pro Ala Asp Gln Ser Val Pro Ala Gly Gly Thr Ala Thr Phe  
325 330 335  
Glu Cys Thr Leu Val Gly Gln Pro Ser Pro Ala Tyr Phe Trp Ser Lys  
340 345 350  
Glu Gly Gln Gln Asp Leu Leu Phe Pro Ser Tyr Val Ser Ala Asp Gly  
355 360 365  
Arg Thr Lys Val Ser Pro Thr Gly Thr Leu Thr Ile Glu Glu Val Arg  
370 375 380  
Gln Val Asp Glu Gly Ala Tyr Val Cys Ala Gly Met Asn Ser Ala Gly  
385 390 395 400  
Ser Ser Leu Ser Lys Ala Ala Leu Lys Val Thr Thr Lys Ala Val Thr  
405 410 415  
Gly Asn Thr Pro Ala Lys Pro Pro Pro Thr Ile Glu His Gly His Gln  
420 425 430  
Asn Gln Thr Leu Met Val Gly Ser Ser Ala Ile Leu Pro Cys Gln Ala  
435 440 445  
Ser Gly Lys Pro Thr Pro Gly Ile Ser Trp Leu Arg Asp Gly Leu Pro  
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Ile Asp Ile Thr Asp Ser Arg Ile Ser Gln His Ser Thr Gly Ser Leu  
465 470 475 480  
His Ile Ala Asp Leu Lys Lys Pro Asp Thr Gly Val Tyr Thr Cys Ile  
485 490 495  
Ala Lys Asn Glu Asp Gly Glu Ser Thr Trp Ser Ala Ser Leu Thr Val  
500 505 510  
Glu Asp His Thr Ser Asn Ala Gln Phe Val Arg Met Pro Asp Pro Ser  
515 520 525  
Asn Phe Pro Ser Ser Pro Thr Gln Pro Ile Ile Val Asn Val Thr Asp  
530 535 540  
Thr Glu Val Glu Leu His Trp Asn Ala Pro Ser Thr Ser Gly Ala Gly  
545 550 555 560  
Pro Ile Thr Gly Tyr Ile Ile Gln Tyr Tyr Ser Pro Asp Leu Gly Gln  
565 570 575  
Thr Trp Phe Asn Ile Pro Asp Tyr Val Ala Ser Thr Glu Tyr Arg Ile  
580 585 590

Lys Gly Leu Lys Pro Ser His Ser Tyr Met Phe Val Ile Arg Ala Glu  
 595 600 605  
 Asn Glu Lys Gly Ile Gly Thr Pro Ser Val Ser Ser Ala Leu Val Thr  
 610 615 620  
 Thr Ser Lys Pro Ala Ala Gln Val Ala Leu Ser Asp Lys Asn Lys Met  
 625 630 635 640  
 Asp Met Ala Ile Ala Glu Lys Arg Leu Thr Ser Glu Gln Leu Ile Lys  
 645 650 655  
 Leu Glu Glu Val Lys Thr Ile Asn Ser Thr Ala Val Arg Leu Phe Trp  
 660 665 670  
 Lys Lys Arg Lys Leu Glu Glu Leu Ile Asp Gly Tyr Tyr Ile Lys Trp  
 675 680 685  
 Arg Gly Pro Pro Arg Thr Asn Asp Asn Gln Tyr Val Asn Val Thr Ser  
 690 695 700  
 Pro Ser Thr Glu Asn Tyr Val Val Ser Asn Leu Met Pro Phe Thr Asn  
 705 710 715 720  
 Tyr Glu Phe Phe Val Ile Pro Tyr His Ser Gly Val His Ser Ile His  
 725 730 735  
 Gly Ala Pro Ser Asn Ser Met Asp Val Leu Thr Ala Glu Ala Pro Pro  
 740 745 750  
 Ser Leu Pro Pro Glu Asp Val Arg Ile Arg Met Leu Asn Leu Thr Thr  
 755 760 765  
 Leu Arg Ile Ser Trp Lys Ala Pro Lys Ala Asp Gly Ile Asn Gly Ile  
 770 775 780  
 Leu Lys Gly Phe Gln Ile Val Ile Val Gly Gln Ala Pro Asn Asn Asn  
 785 790 795 800  
 Arg Asn Ile Thr Thr Asn Glu Arg Ala Ala Ser Val Thr Leu Phe His  
 805 810 815  
 Leu Val Thr Gly Met Thr Tyr Lys Ile Arg Val Ala Ala Arg Ser Asn  
 820 825 830  
 Gly Gly Val Gly Val Ser His Gly Thr Ser Glu Val Ile Met Asn Gln  
 835 840 845  
 Asp Thr Leu Glu Lys His Leu Ala Ala Gln Gln Glu Asn Glu Ser Phe  
 850 855 860  
 Leu Tyr Gly Leu Ile Asn Lys Ser His Val Pro Val Ile Val Ile Val  
 865 870 875 880  
 Ala Ile Leu Ile Ile Phe Val Val Ile Ile Ile Ala Tyr Cys Tyr Trp  
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           20                  25                  30  
 Pro Thr Ile Gln Trp Phe Lys Asp Gly Arg Glu Leu Lys Thr Asp Thr  
           35                  40                  45  
 Gly Ser His Arg Ile Met Leu Pro Ala Gly Gly Leu Phe Phe Leu Lys  
   50                  55                  60  
 Val Ile His Ser Arg Arg Glu Ser Asp Ala Gly Thr Tyr Trp Cys Glu  
   65                  70                  75                  80  
 Ala Lys Asn Glu Phe Gly Val Ala Arg Ser Arg Asn Ala Thr Leu Gln  
           85                  90                  95  
 Val Ala Val Leu Arg Asp Glu Phe Arg Leu Glu Pro Ala Asn Thr Arg  
          100                 105                 110  
 Val Ala Gln Gly Glu Val Ala Leu Met Glu Cys Gly Ala Pro Arg Gly  
          115                 120                 125  
 Ser Pro Glu Pro Gln Ile Ser Trp Arg Lys Asn Gly Gln Thr Leu Asn  
          130                 135                 140  
 Leu Val Gly Asn Lys Arg Ile Arg Ile Val Asp Gly Gly Asn Leu Ala  
  145                 150                 155                 160  
 Ile Gln Glu Ala Arg Gln Ser Asp Asp Gly Arg Tyr Gln Cys Val Val  
          165                 170                 175  
 Lys Asn Val Val Gly Thr Arg Glu Ser Ala Thr Ala Phe Leu Lys Val  
          180                 185                 190  
 His Val Arg Pro Phe Leu Ile Arg Gly Pro Gln Asn Gln Thr Ala Val  
          195                 200                 205  
 Val Gly Ser Ser Val Val Phe Gln Cys Arg Ile Gly Gly Asp Pro Leu  
          210                 215                 220  
 Pro Asp Val Leu Trp Arg Arg Thr Ala Ser Gly Gly Asn Met Pro Leu  
  225                 230                 235                 240  
 Arg Lys Phe Ser Trp Leu His Ser Ala Ser Gly Arg Val His Val Leu  
          245                 250                 255  
 Glu Asp Arg Ser Leu Lys Leu Asp Asp Val Thr Leu Glu Asp Met Gly  
          260                 265                 270

Glu Tyr Thr Cys Glu Ala Asp Asn Ala Val Gly Gly Ile Thr Ala Thr  
 275 280 285  
 Gly Ile Leu Thr Val His Ala Pro Pro Lys Phe Val Ile Arg Pro Lys  
 290 295 300  
 Asn Gln Leu Val Glu Ile Gly Asp Glu Val Leu Phe Glu Cys Gln Ala  
 305 310 315 320  
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 325 330 335  
 Ser Leu Leu Leu Pro Gly Tyr Arg Asp Gly Arg Met Glu Val Thr Leu  
 340 345 350  
 Thr Pro Glu Gly Arg Ser Val Leu Ser Ile Ala Arg Phe Ala Arg Glu  
 355 360 365  
 Asp Ser Gly Lys Val Val Thr Cys Asn Ala Leu Asn Ala Val Gly Ser  
 370 375 380  
 Val Ser Ser Arg Thr Val Val Ser Val Asp Thr Gln Phe Glu Leu Pro  
 385 390 395 400  
 Pro Pro Ile Ile Glu Gln Gly Pro Val Asn Gln Thr Leu Pro Val Lys  
 405 410 415  
 Ser Ile Val Val Leu Pro Cys Arg Thr Leu Gly Thr Pro Val Pro Gln  
 420 425 430  
 Val Ser Trp Tyr Leu Asp Gly Ile Pro Ile Asp Val Gln Glu His Glu  
 435 440 445  
 Arg Arg Asn Leu Ser Asp Ala Gly Ala Leu Thr Ile Ser Asp Leu Gln  
 450 455 460  
 Arg His Glu Asp Glu Gly Leu Tyr Thr Cys Val Ala Ser Asn Arg Asn  
 465 470 475 480  
 Gly Lys Ser Ser Trp Ser Gly Tyr Leu Arg Leu Asp Thr Pro Thr Asn  
 485 490 495  
 Pro Asn Ile Lys Phe Phe Arg Ala Pro Glu Leu Ser Thr Tyr Pro Gly  
 500 505 510  
 Pro Pro Gly Lys Pro Gln Met Val Glu Lys Gly Glu Asn Ser Val Thr  
 515 520 525  
 Leu Ser Trp Thr Arg Ser Asn Lys Val Gly Gly Ser Ser Leu Val Gly  
 530 535 540  
 Tyr Val Ile Glu Met Phe Gly Lys Asn Glu Thr Asp Gly Trp Val Ala  
 545 550 555 560  
 Val Gly Thr Arg Val Gln Asn Thr Thr Phe Thr Gln Thr Gly Leu Leu  
 565 570 575  
 Pro Gly Val Asn Tyr Phe Phe Leu Ile Arg Ala Glu Asn Ser His Gly  
 580 585 590



Leu Ser Leu Pro Ser Pro Met Ser Glu Pro Ile Thr Val Gly Thr Arg  
 595 600 605  
 Tyr Phe Asn Ser Gly Leu Asp Leu Ser Glu Ala Arg Ala Ser Leu Leu  
 610 615 620  
 Ser Gly Asp Val Val Glu Leu Ser Asn Ala Ser Val Val Asp Ser Thr  
 625 630 635 640  
 Ser Met Lys Leu Thr Trp Gln Ile Ile Asn Gly Lys Tyr Val Glu Gly  
 645 650 655  
 Phe Tyr Val Tyr Ala Arg Gln Leu Pro Asn Pro Leu Asn Thr Lys Tyr  
 660 665 670  
 Arg Met Leu Thr Ile Leu Asn Gly Gly Gly Ala Ser Ser Cys Thr Ile  
 675 680 685  
 Thr Gly Leu Val Gln Tyr Thr Leu Tyr Glu Phe Phe Ile Val Pro Phe  
 690 695 700  
 Tyr Lys Ser Val Glu Gly Lys Pro Ser Asn Ser Arg Ile Ala Arg Thr  
 705 710 715 720  
 Leu Glu Asp Val Pro Ser Glu Ala Pro Tyr Gly Met Glu Ala Leu Leu  
 725 730 735  
 Leu Asn Ser Ser Ala Val Phe Leu Lys Trp Lys Ala Pro Glu Leu Lys  
 740 745 750  
 Asp Arg His Gly Val Leu Leu Asn Tyr His Val Ile Val Arg Gly Ile  
 755 760 765  
 Asp Thr Ala His Asn Phe Ser Arg Ile Leu Thr Asn Val Thr Ile Asp  
 770 775 780  
 Ala Ala Ser Pro Thr Leu Val Leu Ala Asn Leu Thr Glu Gly Val Met  
 785 790 795 800  
 Tyr Thr Val Gly Val Ala Ala Gly Asn Asn Ala Gly Val Gly Pro Tyr  
 805 810 815  
 Cys Val Pro Ala Thr Leu Arg Leu Asp Pro Ile Thr Lys Arg Leu Asp  
 820 825 830  
 Pro Phe Ile Asn Gln Arg Asp His Val Asn Asp Val Leu Thr Gln Pro  
 835 840 845  
 Trp Phe Ile Ile Ile Leu Gly Ala Ile Leu Ala Val Leu Met Leu Ser  
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<220>  
 <223> human roundabout (robo) 2 partial cDNA

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 gacagtgata gctgggtgcc accattgcca gtacaaactt acttacacca aggtctggaa 180  
 gatgaactgg aagaagatga tgataggggc ccaacacctc ctgttcgagg cgtggcttct 240  
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<220>  
 <223> human roundabout (robo) 2 partial cDNA

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<210> 17  
 <211> 110  
 <212> PRT  
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<220>  
 <223> human roundabout (robo) 2 partial protein

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 Val Glu Gln Gln Glu Asn Gly Tyr Asp Ser Asp Ser Trp Cys Pro Pro  
 35 40 45  
 Leu Pro Val Gln Thr Tyr Leu His Gln Gly Leu Glu Asp Glu Leu Glu  
 50 55 60  
 Glu Asp Asp Asp Arg Val Pro Thr Pro Pro Val Arg Gly Val Ala Ser  
 65 70 75 80  
 Ser Pro Ala Ile Ser Phe Gly Gln Gln Ser Thr Ala Thr Leu Thr Pro  
 85 90 95  
 Ser Pro Arg Glu Glu Met Gln Pro Met Leu Gln Ala Ser Pro  
 100 105 110

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 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human roundabout (robo) 2 partial protein

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                     20                    25                    30  
 Lys Lys His Lys Gly Gly  
                     35

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<220>  
 <223> H-Robo1 (502-651)

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                     20                    25                    30  
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<220>  
 <223> EST:yu23d11 H77734

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 Gly Glu Pro Ala Val Met Glu Cys Gln Pro Pro Arg Gly His Pro Glu  
                     20                    25                    30  
 Pro Thr Ile Ser Trp Lys Lys Asp Gly Ser Pro Leu Asp Asp Lys Asp  
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 Glu Arg  
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 <212> DNA  
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 <220>  
 <223> H-Robol (502-651)  
  
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 <210> 22  
 <211> 50  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <223> EST:yu23d11 H77734  
  
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 <213> Homo sapiens  
  
 <220>  
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 35 40 45  
 Ser Ser Val Thr Gly Ser Met Ile Asn Gly Trp Gly Ser Ala Ser Glu  
 50 55 60  
 Glu Asp Asn Ile Ser Ser Gly Arg Ser Ser Val Ser Ser Ser Asp Gly  
 65 70 75 80

Ser Phe Phe Thr Asp Ala Asp Phe Ala Gln Ala Val Ala Ala Ala Ala  
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 Glu Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln Met Gln Asp Ala Ala  
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 Gly Arg Arg His Phe His Ala Ser Gln Cys Pro Arg Pro Thr Ser Pro  
                             115                            120                            125  
 Val Ser Thr Asp Ser Asn Met Ser Ala Ala Val Met Gln Lys Thr Arg  
             130                            135                            140  
 Pro Ala Lys Lys Leu Lys His Gln Pro Gly His Leu Arg Arg Glu Thr  
     145                            150                            155                            160  
 Tyr Thr Asp Asp Leu Pro Pro Pro Pro Val Pro Pro Pro Ala Ile Lys  
                             165                            170                            175  
 Ser Pro Thr Ala Gln Ser Lys Thr Gln Leu Glu Val Arg Pro Val Val  
                             180                            185                            190  
 Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr Asp Lys  
             195                            200                            205

<210> 25  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <223> EST:yq76e12 H52936

<400> 25  
 Gly Pro Leu Val Ser Asp Met Asp Thr Asp Ala Pro Glu Glu Glu Glu  
     1                            5                            10                            15  
 Asp Glu Ala Asp Met Glu Val Ala Lys Met Gln Thr Arg Leu Leu Leu  
             20                            25                            30  
 Arg Gly Leu Glu Gln Thr Pro Ala Ser Ser Val Gly Asp Leu Glu Ser  
             35                            40                            45  
 Ser Val Thr Gly Ser Met Ile Asn Gly Trp Gly Ser Ala Ser Glu Glu  
             50                            55                            60  
 Asp Asn Ile Ser Ser Gly Arg Ser Ser Val Ser Ser Ser Asp Gly Ser  
     65                            70                            75                            80  
 Phe Phe Thr Asp Ala Asp Phe Ala Gln Ala Val Ala Ala Ala Ala Glu  
             85                            90                            95  
 Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln Met Gln Asp Ala Ala Gly  
             100                            105                            110  
 Arg Arg His Phe His Ala Phe Gln Cys Pro Arg Pro Thr Ser Pro Val  
             115                            120                            125  
 Phe Thr Asp Ser Asn Met  
     130

<210> 26  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> EST:yq76e12 H52937

<220>  
 <221> MOD\_RES  
 <222> (1)..(6)  
 <223> Xaa = unknown amino acid

<400> 26  
 Xaa Ala Ala Thr Ala Xaa Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln  
           1                  5                  10                  15  
 Met Arg Asp Ala Ala Gly Arg Arg His Phe His Ala Ser Gln Cys Pro  
                   20                  25                  30  
 Arg Pro Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser Ala Ala Val  
                   35                  40                  45  
 Met Gln Lys Thr Arg Pro Ala Lys Lys Leu Lys His Gln Pro Gly His  
           50                  55                  60  
 Leu Arg Arg Glu Thr Tyr Thr Asp Asp Leu Pro Pro Pro Pro Val Pro  
           65                  70                  75                  80  
 Pro Pro Ala Ile Lys Ser Pro Thr Ala Gln Ser Lys Thr Gln Leu Glu  
                   85                  90                  95  
 Val Arg Pro Val Val Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr  
           100                  105                  110  
 Asp Lys

<210> 27  
 <211> 303  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:hybridization  
           probe for human roundabout 1 immunoglobulin domain  
           #1

<400> 27  
 ccacctcgca ttgttgaaca cccttcagac ctgattgtct caaaaggaga acctgcaact 60  
 ttgaactgca aagctgaagg ccgcccacac cccactattg aatggtacaa agggggagag 120  
 agagtggaga cagacaaaga tgaccctcgc tcacaccgaa tgttgctgcc gagtggatct 180  
 ttatttttct tacgtatagt acatggacgg aaaagtagac ctgatgaagg agtctatgtc 240  
 tgtgtagcaa ggaattacct tggagaggct gtgagccaca atgcatcgct ggaagtagcc 300  
 ata 303

<210> 28  
 <211> 275  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybridization  
probe for human roundabout 1 immunoglobulin domain  
#2

<400> 28

```
cttcgggatg acttcagaca aaacccttcg gatgtcatgg ttgcagtagg agagcctgca 60
gtaatggaat gccaacctcc acgaggccat cctgagccca ccatttcatg gaagaaagat 120
ggctctccac tggatgataa agatgaaaga ataactatac gaggaggaaa gctcatgatc 180
acttacaccc gtaaaagtga cgctggcaaa tatgtttgtg ttggtaccaa tatggttggg 240
gaacgtgaga gtgaagtagc cgagctgact gtctt 275
```

<210> 29

<211> 273

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybridization  
probe for human roundabout 1 immunoglobulin domain  
#3

<400> 29

```
agagagacca tcatttgtga agagaccag taacttggca gtaactgtgg atgacagtgc 60
agaatttaaa tgtgaggccc gaggtgacct tgtacctaca gtacgatgga ggaaagatga 120
tggagagctg cccaaatcca gatatgaaat ccgagatgat cataccttga aaattaggaa 180
ggtgacagct ggtgacatgg gtccatacac ttgtgttgca gaaaatatgg tgggcaaagc 240
tgaagcatct gctactctga ctgttcaaga acc 273
```

<210> 30

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybridization  
probe for human roundabout 1 immunoglobulin domain  
#4

<400> 30

```
ccacattttg ttgtgaaacc ccgtgaccag gttgttgctt tgggacggac tgtaactttt 60
cagtgtgaag caaccggaat tcctcaacca gctattttct ggaggagaga agggagtcag 120
aatctacttt tctcatatca accaccacag tcatccagcc gattttcagt ctcccagact 180
ggcgacctca caattactaa tgtccagcga tctgatgttg gttattacat ctgccagact 240
ttaaattgtt ctggaagcat catcacaag gcatatttgg aagttacaga tgtgattgca 300
```

<210> 31

<211> 286

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybridization  
probe for human roundabout 1 immunoglobulin domain  
#5

<400> 31

```
gatcggcctc ccccagttat tcgacaaggt cctgtgaatc agactgtagc cgtggatggc 60
```

```

actttcgtcc tcagctgtgt ggccacaggc agtccagtgc ccaccattct gtggagaaaag 120
gatggagtcc tcgtttcaac ccaagactct cgaatcaaac agttggagaa tggagtactg 180
cagatccgat atgctaagct ggggtgatact ggtcgggtaca cctgcattgc atcaaccccc 240
agtgggtgaag caacatggag tgcttacatt gaagttcaag aatttg 286

```

```

<210> 32
<211> 297
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:hybridization
      probe for human roundabout 1 fibronectin domain #1

```

```

<400> 32
gagttccagt tcagcctcca agacctactg acccaaattt aatccctagt gccccatcaa 60
aacctgaagt gacagatgtc agcagaaata cagtcacatt atcgtggcaa ccaaatttga 120
attcaggagc aactccaaca tcttatatta tagaagcctt cagccatgca tctggtagca 180
gctggcagac cgtagcagag aatgtgaaaa cagaaacatc tgccattaaa ggactcaaac 240
ctaattgcaat ttaccttttc cttgtgaggg cagctaattgc atatggaatt agtgatc 297

```

```

<210> 33
<211> 351
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:hybridization
      probe for human roundabout 1 fibronectin domain #2

```

```

<400> 33
caagccaaat atcagatcca gtgaaaacac aagatgtcct accaacaagt caggggggtg 60
accacaagca ggtccagaga gagctgggaa atgctgttct gcacctccac aacccccaccg 120
tcctttcttc ctcttccatc gaagtgcact ggacagtaga tcaacagtct cagtatatac 180
aaggatataa aattctctat cggccatctg gagccaacca cggagaatca gactgggttag 240
tttttgaaat gaggacgcca gccaaaaaca gtgtggtaat ccctgatctc agaaagggag 300
tcaactatga aattaaggct cgcccttttt ttaatgaatt tcaaggagca g 351

```

```

<210> 34
<211> 305
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:hybridization
      probe for human roundabout 1 fibronectin domain #3

```

```

<400> 34
atagtgaat caagtttgcc aaaaccctgg aagaagcacc cagtgcccca cccaaggtg 60
taactgtatc caagaatgat ggaaacggaa ctgcaattct agttagttag cagccacctc 120
cagaagacac tcaaaatgga atggtccaag agtataaggt ttggtgtctg ggcaatgaaa 180
ctcgatacca catcaacaaa acagtggatg gttccacctt ttccgtgggc attccctttc 240
ttgttcctgg aatccgatac agtgtggaag tggcagccag cactgggggt ggggtctggg 300
taaag 305

```



<210> 35  
 <211> 100  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:hybridization  
       probe for human roundabout 1 transmembrane domain  
  
 <400> 35  
 agatttcaga tgtggtgaag cagccggcct tcatagcagg tattggagca gcctggtgga 60  
 tcacctcat ggtcttcagc atctggcttt atcgacaccg 100  
  
 <210> 36  
 <211> 100  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:hybridization  
       probe for human roundabout 1 cytoplasmic motif #1  
  
 <400> 36  
 aatctgaagg atgggcgttt tgtcaatcca tcagggcagc ctactcctta cgccaccact 60  
 cagctcatcc agtcaaact cagcaacaac atgaacaatg 100  
  
 <210> 37  
 <211> 100  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:hybridization  
       probe for human roundabout 1 cytoplasmic motif #2  
  
 <400> 37  
 cccaaggtac caaaacaggg tggcatgaac tgggcagacc tgcttcctcc tccccagca 60  
 catcctctc cacacagcaa tagcgaagag tacaacattt 100  
  
 <210> 38  
 <211> 100  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:hybridization  
       probe for human roundabout 1 cytoplasmic motif #3  
  
 <400> 38  
 ccagccagga catctgcgca gagaaaccta cacagatgat cttccaccac ctctgtgcc 60  
 gccacctgct ataaagtcac ctactgcca atccaagaca 100  
  
 <210> 39  
 <211> 273  
 <212> DNA  
 <213> Artificial Sequence

```

<220>
<223> Description of Artificial Sequence:hybridization
      probe for human roundabout 2 immunoglobulin domain
      #4

<400> 39
cagattgttg ctcaaggtcg aacagtgaca tttccctgtg aaactaaagg aaaccacag 60
ccagctgttt tttggcagaa agaaggcagc cagaacctac ttttccaaa ccaaccccag 120
cagcccaaca gtagatgctc agtgtcacca actggagacc tcacaatcac caacattcaa 180
cgttccgacg cgggttacta catctgccag gctttaactg tggcaggaag catttttagca 240
aaagctcaac tggaggttac tgatgttttg aca                                     273

<210> 40
<211> 285
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybridization
      probe for human roundabout 2 immunoglobulin domain
      #5

<400> 40
gatagacctc cacctataat tctacaaggc ccagccaacc aaacgctggc agtggatggt 60
acagcgttac tgaaatgtaa agccactggt gatcctcttc ctgtaattag ctgggttaaag 120
gagggattta cttttccggg tagagatcca agagcaacaa ttcaagagca aggcacactg 180
cagattaaga atttacggat ttctgatact ggcacttata cttgtgtggc tacaagttca 240
agtggagagg cttcctggag tgcagtgtcg gatgtgacag agtct                                     285

<210> 41
<211> 296
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybridization
      probe for human roundabout 2 fibronectin domain #1

<400> 41
ggagcaacaa tcagtaaaaa ctatgattta agtgacctgc cagggccacc atccaaaccg 60
caagtcactg atgttactaa gaacagtgtc accttgtcct ggcagccagg taccocctgga 120
acccttccag caagtgcata tatcattgag gctttcagcc aatcagtgag caacagctgg 180
cagaccgtgg caaaccatgt aaagaccacc ctctatactg taagaggact gcggcccaat 240
acaatctact tattcatggt cagagcgatc aacccaagg tytcagtgc ccaagt       296

<210> 42
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human
      roundabout 1 immunoglobulin domain #1 PCR forward
      primer

<400> 42
ccacctcgca ttgttgaaca cccttcagac

```

30

<210> 43  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
         roundabout 1 immunoglobulin domain #1 PCR reverse  
         primer  
  
 <400> 43  
 atggctactt ccagcgatgc attgtggctc 30  
  
  
 <210> 44  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
         roundabout 1 immunoglobulin domain #2 PCR forward  
         primer  
  
 <400> 44  
 cttcgggatg acttcagaca aaacccttcg 30  
  
  
 <210> 45  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
         roundabout 1 immunoglobulin domain #2 PCR reverse  
         primer  
  
 <400> 45  
 taagacagtc agctcggcta cttcactctc 30  
  
  
 <210> 46  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
         roundabout 1 immunoglobulin domain #3 PCR forward  
         primer  
  
 <400> 46  
 agagagacca tcatttgtga agagaccag 30  
  
  
 <210> 47  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 immunoglobulin domain #3 PCR reverse  
 primer

<400> 47  
 aggttcttga acagtcagag tagcagatgc 30

<210> 48  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 immunoglobulin domain #4 PCR forward  
 primer

<400> 48  
 ccacattttg ttgtgaaacc ccgtgaccag 30

<210> 49  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 immunoglobulin domain #4 PCR reverse  
 primer

<400> 49  
 tgcaatcaca tctgtaactt ccaaatatgc 30

<210> 50  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 immunoglobulin domain #5 PCR forward  
 primer

<400> 50  
 atcggcctcc ccagttatt cgacaaggtc 30

<210> 51  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 immunoglobulin domain #5 PCR reverse  
 primer

<400> 51  
 caaattcttg aacttcaatg taagcactcc 30

<210> 52  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 fibronectin domain #1 PCR forward  
 primer

<400> 52  
 gagttccagt tcagcctcca agacctactg 30

<210> 53  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 fibronectin domain #1 PCR reverse  
 primer

<400> 53  
 tcactaattc catatgcatt agctgccctc 30

<210> 54  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 fibronectin domain #2 PCR forward  
 primer

<400> 54  
 caagccaaat atcagatcca gtgaaaacac 30

<210> 55  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 fibronectin domain #2 PCR reverse  
 primer

<400> 55  
 atctgctcct tgaaattcat taaaaaaagg 30

<210> 56  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
         roundabout 1 fibronectin domain #3 PCR forward  
         primer  
  
 <400> 56  
 atagtgaat caagtttgcc aaaaccctg 29  
  
 <210> 57  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
         roundabout 1 fibronectin domain #3 PCR reverse  
         primer  
  
 <400> 57  
 ctctttaccc cagaccagc ccagtgctg 30  
  
 <210> 58  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
         roundabout 1 transmembrane domain PCR forward  
         primer  
  
 <400> 58  
 ggaccaagtc agcctcgctc agcagatttc 30  
  
 <210> 59  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
         roundabout 1 transmembrane domain PCR reverse  
         primer  
  
 <400> 59  
 actagtaagt ccgtttctct tcttgcggtg 30  
  
 <210> 60  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 cytoplasmic motif #1 PCR forward  
 primer  
  
 <400> 60  
 ctgaaggatg ggcgttttgt caatccatc 29  
  
 <210> 61  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 cytoplasmic motif #1 PCR reverse  
 primer  
  
 <400> 61  
 gtcccagtgg tttccagtgc ttctcgccag 30  
  
 <210> 62  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 cytoplasmic motif #2 PCR forward  
 primer  
  
 <400> 62  
 ggcacaagaa aggggcaaga acacccaagg 30  
  
 <210> 63  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 cytoplasmic motif #2 PCR reverse  
 primer  
  
 <400> 63  
 atagctttca tctacagaaa tgttgtactc 30  
  
 <210> 64  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 cytoplasmic motif #3 PCR forward  
 primer

<400> 64  
 accagaccag ccaagaaact gaaacaccag 30

<210> 65  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:human  
 roundabout 1 cytoplasmic motif #3 PCR reverse  
 primer

<400> 65  
 gtacttccag ctgtgtcttg gattgggcag 30

<210> 66  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:human  
 roundabout 2 immunoglobulin domain #4 PCR forward  
 primer

<400> 66  
 gttgctcaag gtcgaacagt gacatttccc 30

<210> 67  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:human  
 roundabout 2 immunoglobulin domain #4 PCR reverse  
 primer

<400> 67  
 tgtcaaaaca tcagtaacct ccagttgagc 30

<210> 68  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:human  
 roundabout 2 immunoglobulin domain #5 PCR forward  
 primer

<400> 68  
 gatagacctc cacctataat tctacaaggc 30



<210> 69  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
         roundabout 2 immunoglobulin domain #5 PCR reverse  
         primer  
  
 <400> 69  
 gactctgtca catccagcac tgcactccag 30  
  
  
 <210> 70  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
         roundabout 2 fibronectin domain #1 PCR forward  
         primer  
  
 <400> 70  
 caatcagtaa aaactatgat ttaagtg 27  
  
  
 <210> 71  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
         roundabout 2 fibronectin domain #1 PCR reverse  
         primer  
  
 <400> 71  
 tcgctctgac catgaataag tagattg 27  
  
  
 <210> 72  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:Drosophila  
         roundabout-I conserved cytoplasmic motif #1  
  
 <400> 72  
 Pro Asp Asn Pro Thr Pro Tyr Ala Thr Thr Met Ile Ile Gly Thr Ser  
   1                  5                  10                  15  
 Ser

<210> 73  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:human  
         roundabout-I conserved cytoplasmic motif #1  
  
 <400> 73  
 Ser Gly Gln Pro Thr Pro Tyr Ala Thr Thr Gln Leu Ile Gln Ser Asn  
     1                    5                    10                    15  
  
 Leu  
  
 <210> 74  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:Drosophila  
         roundabout-II conserved cytoplasmic motif #1  
  
 <400> 74  
 Asn Ala Ser Pro Ala Pro Tyr Ala Thr Ser Ser Ile Leu Ser Pro His  
     1                    5                    10                    15  
  
 Gln  
  
 <210> 75  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:C. elegans  
         roundabout conserved cytoplasmic motif #1  
  
 <400> 75  
 His Asp Asp Pro Ser Pro Tyr Ala Thr Thr Thr Leu Val Leu Ser Asn  
     1                    5                    10                    15  
  
 Gln  
  
 <210> 76  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:consensus  
         roundabout conserved cytoplasmic motif #1  
  
 <220>  
 <221> MOD\_RES  
 <222> (8)  
 <223> Xaa = any amino acid

<220>  
<221> MOD\_RES  
<222> (9)..(10)  
<223> Xaa = Ile, Leu or Val

<400> 76  
Pro Thr Pro Tyr Ala Thr Thr Xaa Xaa Xaa  
1 5 10

<210> 77  
<211> 22  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Drosophila  
roundabout-I conserved cytoplasmic motif #2

<400> 77  
Ile Asn Trp Ser Glu Phe Leu Pro Pro Pro Pro Glu His Pro Pro Pro  
1 5 10 15

Ser Ser Thr Tyr Gly Tyr  
20

<210> 78  
<211> 23  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:human  
roundabout-I conserved cytoplasmic motif #2

<400> 78  
Met Asn Trp Ala Asp Leu Leu Pro Pro Pro Pro Ala His Pro Pro Pro  
1 5 10 15

His Ser Asn Ser Glu Glu Tyr  
20

<210> 79  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:human  
roundabout-II conserved cytoplasmic motif #2

<400> 79  
Ser Thr Trp Ala Asn Val Pro Leu Pro Pro Pro Pro Val Gln Pro Leu  
1 5 10 15

Pro Gly Thr Glu Leu Glu His Tyr  
20

<210> 80  
 <211> 22  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:C. elegans  
         roundabout conserved cytoplasmic motif #2  
  
 <400> 80  
 Lys Thr Leu Met Asp Phe Ile Pro Pro Pro Pro Ser Asn Pro Pro Pro  
     1                    5                    10                    15  
 Pro Gly Gly His Val Tyr  
                     20

<210> 81  
 <211> 23  
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         roundabout conserved cytoplasmic motif #2

<220>  
 <221> MOD\_RES  
 <222> (3)..(5)  
 <223> Xaa = any amino acid

<220>  
 <221> MOD\_RES  
 <222> (6)..(7)  
 <223> Xaa = hydrophobic amino acid

<220>  
 <221> MOD\_RES  
 <222> (12)..(22)  
 <223> Xaa = any amino acid

<400> 81  
 Asn Trp Xaa Xaa Xaa Xaa Xaa Pro Pro Pro Pro Xaa Xaa Pro Pro Pro  
     1                    5                    10                    15  
 Xaa Ser Xaa Xaa Xaa Xaa Tyr  
                     20

<210> 82  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Drosophila  
         roundabout-I conserved cytoplasmic motif #3

<400> 82  
Pro Ser Pro Met Gln Pro Pro Pro Pro Val Pro Val Pro Glu Gly Trp  
1 5 10 15

Tyr

<210> 83  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:human  
roundabout-I conserved cytoplasmic motif #3

<400> 83  
Tyr Thr Asp Asp Leu Pro Pro Pro Pro Val Pro Pro Pro Ala Ile Lys  
1 5 10 15

Ser Pro

<210> 84  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mouse  
roundabout-I conserved cytoplasmic motif #3

<400> 84  
Tyr Ala Asp Asp Leu Pro Pro Pro Pro Val Pro Pro Pro Ala Ile Lys  
1 5 10 15

Ser Pro

<210> 85  
<211> 18  
<212> PRT  
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<220>  
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roundabout conserved cytoplasmic motif #3

<400> 85  
Arg Ala Pro Ala Met Pro Thr Asn Pro Val Pro Pro Glu Pro Pro Ala  
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Arg Tyr

<210> 86  
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<212> PRT  
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<220>  
 <223> Description of Artificial Sequence:consensus  
 roundabout conserved cytoplasmic motif #3  
  
 <400> 86  
 Pro Pro Pro Pro Val Pro Pro Pro  
 1 5  
  
 <210> 87  
 <211> 4  
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 Enabled protein  
  
 <400> 87  
 Leu Pro Pro Pro  
 1  
  
 <210> 88  
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 primer specific for region flanking CfoI  
 polymorphism  
  
 <400> 88  
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 <210> 89  
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 primer specific for region flanking CfoI  
 polymorphism  
  
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 <210> 90  
 <211> 42  
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 <223> Description of Artificial Sequence:D-robo ORF PCR  
 amplification primer

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<210> 91  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:D-robo ORF PCR  
amplification primer

<400> 91  
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<210> 92  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:six histidine  
fusion protein tag

<400> 92  
His His His His His His  
1 5